

SEQ ID NO 89
 LENGTH: 775
 TYPE: PRT
 ORGANISM: *Pyrococcus furiosus*
 SEQUENCE: 89

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Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1           5           10           15
Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
20           25           30
Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35           40           45
Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50           55           60
Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65           70           75           80
Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
85           90           95
Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100          105          110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115          120          125
Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130          135          140
Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145          150          155          160
Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165          170          175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180          185          190
Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195          200          205
Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210          215          220
Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225          230          235          240
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245          250          255
His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260          265          270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275          280          285
Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
290          295          300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305          310          315          320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
325          330          335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340          345          350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
355          360          365
Pro Asn Lys Pro Ser Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
370          375          380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385          390          395          400
Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
405          410          415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr

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420										425					430							
Asp	Ile	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Ile	Pro	Gly							
		435						440					445									
Phe	Ile	Pro	Ser	Leu	Leu	Gly	His	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Ile							
		450				455						460										
Lys	Thr	Lys	Met	Lys	Glu	Thr	Gln	Asp	Pro	Ile	Glu	Lys	Ile	Leu	Leu							
		465			470				475						480							
Asp	Tyr	Arg	Gln	Lys	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Phe	Tyr	Gly							
				485					490					495								
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu							
			500					505					510									
Ser	Val	Thr	Ala	Trp	Gly	Arg	Lys	Tyr	Ile	Glu	Leu	Val	Trp	Lys	Glu							
		515					520					525										
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly							
		530			535						540											
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Glu	Ser	Glu	Glu	Ile	Lys	Lys	Lys							
				550					555						560							
Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu							
			565					570						575								
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys							
			580					585					590									
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Val	Ile	Thr	Arg	Gly							
		595					600					605										
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln							
		610				615					620											
Ala	Arg	Val	Leu	Glu	Thr	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala							
				630					635						640							
Val	Arg	Ile	Val	Lys	Glu	Val	Ile	Gln	Lys	Leu	Ala	Asn	Tyr	Glu	Ile							
			645						650					655								
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His							
			660				665						670									
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Lys	Leu	Ala							
		675					680					685										
Ala	Lys	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val							
		690				695					700											
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Asn	Arg	Ala	Ile	Leu	Ala	Glu	Glu							
				710					715					720								
Tyr	Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn							
				725					730					735								
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Gly	Phe	Gly	Tyr	Arg							
			740					745					750									
Lys	Glu	Asp	Leu	Arg	Tyr	Gln	Lys	Thr	Arg	Gln	Val	Gly	Leu	Thr	Ser							
		755					760					765										
Trp	Leu	Asn	Ile	Lys	Lys	Ser																
		770				775																

Examiner's alignment::

BRS	L1	63480	polymerase	USPAT	2010/09/29 14:05	
BRS	L2	24	11 and v93	USPAT	2010/09/29 14:05	
BRS	L3	38105	11 and (valine mutation)	USPAT	2010/09/29 14:14	
BRS	L4	744	11 and (valine.c1m.)	USPAT	2010/09/29 14:14	
BRS	L5	30	14 and polymerase.c1m.	USPAT	2010/09/29 14:15	
BRS	L6	40	valine adj mutation	USPAT	2010/09/29 14:28	
BRS	L7	187	(valine adj mutation) or (valine adj substitution)	USPAT		
			2010/09/29 14:28			

BRS	L8	139	11 and 17	USPAT	2010/09/29 14:29
BRS	L9	9	18 and polymerase .clm.	USPAT	2010/09/29 14:29
BRS	L10	11437	11 and uracil	USPAT	2010/09/29 14:37
BRS	L11	1197	110 and polymerase.clm.	USPAT	2010/09/29 14:37
BRS	L12	9	15 and uracil	USPAT	2010/09/29 14:38

STN SEARCH:

(FILE 'HOME' ENTERED AT 14:53:01 ON 29 SEP 2010)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, JAPIO, BIOTECHNO' ENTERED AT 14:54:04 ON 29 SEP 2010

L1	1669300	S POLYMERASE
L2	1	S L1 AND V93
L3	5269	S L1 AND URACIL
L4	1	S L1 AND POLYMERASE.TI.
L5	5057	S L1 AND VALINE
L6	13	S L5 AND URACIL
L7	11	DUP REM L6 (2 DUPLICATES REMOVED)
L8	11938	S L1 AND EXONUCLEASE
L9	29	S L8 AND VALINE
L10	14	DUP REM L9 (15 DUPLICATES REMOVED)

ANSWER 10 OF 14 CAPLUS COPYRIGHT 2010 ACS on STN

AN 1999:409781 CAPLUS

DN 131:225462

TI A Single Tyrosine Prevents Insertion of Ribonucleotides in the Eukaryotic-type .phi.29 DNA Polymerase

AU Bonnin, Ana; Lazaro, Jose M.; Blanco, Luis; Salas, Margarita

CS Centro de Biologia Molecular "Severo Ochoa" (CSIC-UAM), Universidad

Autonoma, Canto Blanco, Madrid, 28049, Spain

SO Journal of Molecular Biology (1999), 290(1), 241-251

CODEN: JMOBAK; ISSN: 0022-2836

PB Academic Press

DT Journal

LA English

AB Three conserved motifs (named A, B and C) have been proposed to form the polymn. active site in all classes of DNA-dependent polymerases. In eukaryotic-type (.alpha.-like) DNA polymerases, motif A is characterized by the consensus "Dx2SLYP". Mutants in .phi.29 DNA polymerase residue Tyr254 of this conserved motif had been previously shown to be affected in dNTP binding. Here, we show that a single substitution of Tyr254 into a valine residue enables the enzyme to incorporate ribonucleotide substrates, without affecting its wild-type affinity for dNTPs. Whereas the wild-type enzyme preferred dNTPs more than two million-fold over rNTPs, the mutation of Tyr254 into valine reduced the discrimination for rNTPs up to 1000-fold. In addn. to this discrimination mechanism, based on sugar selection, .phi.29 DNA polymerase is very inefficient when extending an RNA primer terminus, allowing its exonucleolytic degrdn. These results indicate that the Tyr254 of .phi.29 DNA polymerase is responsible for the discrimination against the 2'-OH group of an incoming ribonucleotide. This is the first time that the invariant tyrosine residue of motif A is

involved in ribo- vs. deoxyribonucleotide discrimination in an
 eukaryotic-type DNA polymerase. (c) 1999 Academic Press.
 OSC.G 36 THERE ARE 36 CAPLUS RECORDS THAT CITE THIS RECORD (36 CITINGS)
 RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

SEQ ID NO 108

LENGTH: 882

TYPE: PRT

ORGANISM: *Sulfolobus solfataricus*

SEQUENCE: 108

Met	Thr	Lys	Gln	Leu	Thr	Leu	Phe	Asp	Ile	Pro	Ser	Ser	Lys	Pro	Ala	1	5	10	15
Lys	Ser	Glu	Gln	Asn	Thr	Gln	Gln	Ser	Gln	Ser	Ala	Pro	Val	Glu		20	25	30	
Glu	Lys	Lys	Val	Val	Arg	Arg	Glu	Trp	Leu	Glu	Glu	Ala	Gln	Glu	Asn	35	40	45	
Lys	Ile	Tyr	Phe	Leu	Leu	Gln	Val	Asp	Tyr	Asp	Gly	Lys	Lys	Gly	Lys	50	55	60	
Ala	Val	Cys	Lys	Leu	Phe	Asp	Lys	Glu	Thr	Gln	Lys	Ile	Tyr	Ala	Leu	65	70	75	93
Tyr	Asp	Asn	Thr	Gly	His	Lys	Pro	Tyr	Phe	Leu	Val	Asp	Leu	Glu	Pro	85	90	95	
Asp	Lys	Val	Gly	Lys	Ile	Pro	Lys	Ile	Val	Arg	Asp	Pro	Ser	Phe	Asp	100	105	110	
His	Ile	Glu	Thr	Val	Ser	Lys	Ile	Asp	Pro	Tyr	Thr	Trp	Asn	Lys	Phe	115	120	125	
Lys	Leu	Thr	Lys	Ile	Val	Val	Arg	Asp	Pro	Leu	Ala	Val	Arg	Arg	Leu	130	135	140	
Arg	Asn	Asp	Val	Pro	Lys	Ala	Tyr	Glu	Ala	His	Ile	Lys	Tyr	Phe	Asn	145	150	155	160
Asn	Tyr	Met	Tyr	Asp	Ile	Gly	Leu	Ile	Pro	Gly	Met	Pro	Tyr	Val	Val	165	170	175	
Lys	Asn	Gly	Lys	Leu	Glu	Ser	Val	Tyr	Leu	Ser	Leu	Asp	Glu	Lys	Asp	180	185	190	
Val	Glu	Glu	Ile	Lys	Lys	Ala	Phe	Ala	Asp	Ser	Asp	Glu	Met	Thr	Arg	195	200	205	
Gln	Met	Ala	Val	Asp	Trp	Leu	Pro	Ile	Phe	Glu	Thr	Glu	Ile	Pro	Lys	210	215	220	
Ile	Lys	Arg	Val	Ala	Ile	Asp	Ile	Glu	Val	Tyr	Thr	Pro	Val	Lys	Gly	225	230	235	240
Arg	Ile	Pro	Asp	Ser	Gln	Lys	Ala	Glu	Phe	Pro	Ile	Ile	Ser	Ile	Ala	245	250	255	
Leu	Ala	Gly	Ser	Asp	Gly	Leu	Lys	Lys	Val	Leu	Val	Leu	Asn	Arg	Asn	260	265	270	
Asp	Val	Asn	Glu	Gly	Ser	Val	Lys	Leu	Asp	Gly	Ile	Ser	Val	Glu	Arg	275	280	285	
Phe	Asn	Thr	Glu	Tyr	Glu	Leu	Leu	Gly	Arg	Phe	Phe	Asp	Ile	Leu	Leu	290	295	300	
Glu	Tyr	Pro	Ile	Val	Leu	Thr	Phe	Asn	Gly	Asp	Asp	Phe	Asp	Leu	Pro	305	310	315	320
Tyr	Ile	Tyr	Phe	Arg	Ala	Leu	Lys	Leu	Gly	Tyr	Phe	Pro	Glu	Glu	Ile	325	330	335	
Pro	Ile	Asp	Val	Ala	Gly	Lys	Asp	Glu	Ala	Lys	Tyr	Leu	Ala	Gly	Leu	340	345	350	
His	Ile	Asp	Leu	Tyr	Lys	Phe	Phe	Phe	Asn	Lys	Ala	Val	Arg	Asn	Tyr	355	360	365	
Ala	Phe	Glu	Gly	Lys	Tyr	Asn	Glu	Tyr	Asn	Leu	Asp	Ala	Val	Ala	Lys	370	375	380	
Ala	Leu	Leu	Gly	Thr	Ser	Lys	Val	Lys	Val	Asp	Thr	Leu	Ile	Ser	Phe	385	390	395	400
Leu	Asp	Val	Glu	Lys	Leu	Ile	Glu	Tyr	Asn	Phe	Arg	Asp	Ala	Glu	Ile	405	410	415	
Thr	Leu	Gln	Leu	Thr	Thr	Phe	Asn	Asn	Asp	Leu	Thr	Met	Lys	Leu	Ile				

Val	Leu	Phe	420				Ser	Arg	Ile	Ser	Arg	425				Leu	Gly	Ile	Glu	Glu	430				
			435	440	445	450						455	460	465	470						475	480	485	490	495
Thr	Glu	Ile	Ser	Thr	Trp	Val	Lys	Asn	Leu	Tyr	Tyr	Trp	Glu	His	Arg										
Lys	Arg	Asn	Trp	Leu	Ile	Pro	Leu	Lys	Glu	Glu	Ile	Leu	Ala	Lys	Ser										
465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465	465
Ser	Asn	Ile	Arg	Thr	Ser	Ala	Leu	Ile	Lys	Gly	Lys	Gly	Tyr	Lys	Gly										
Ala	Val	Val	Ile	Asp	Pro	Pro	Ala	Gly	Ile	Phe	Phe	Asn	Ile	Thr	Val										
Leu	Asp	Phe	Ala	Ser	Leu	Tyr	Pro	Ser	Ile	Ile	Arg	Thr	Trp	Asn	Leu										
515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515	515
Ser	Tyr	Glu	Thr	Val	Asp	Ile	Gln	Gln	Cys	Lys	Lys	Pro	Tyr	Glu	Val										
530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530	530
Lys	Asp	Glu	Thr	Gly	Glu	Val	Leu	His	Ile	Val	Cys	Met	Asp	Arg	Pro										
545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545	545
Gly	Ile	Thr	Ala	Val	Ile	Thr	Gly	Leu	Leu	Arg	Asp	Phe	Arg	Val	Lys										
Ile	Tyr	Lys	Lys	Lys	Lys	Lys	Asn	Pro	Asn	Asn	Ser	Glu	Glu	Gln	Lys										
580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580	580
Leu	Leu	Tyr	Asp	Val	Val	Gln	Arg	Ala	Met	Lys	Val	Phe	Ile	Asn	Ala										
595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595
Thr	Tyr	Gly	Val	Phe	Gly	Ala	Glu	Thr	Phe	Pro	Leu	Tyr	Ala	Pro	Ala										
610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610	610
Val	Ala	Glu	Ser	Val	Thr	Ala	Leu	Gly	Arg	Tyr	Val	Ile	Thr	Ser	Thr										
625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625	625
Val	Lys	Lys	Ala	Arg	Glu	Glu	Gly	Leu	Thr	Val	Leu	Tyr	Gly	Asp	Thr										
645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645	645
Asp	Ser	Leu	Phe	Leu																					